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From: Parkin, Jeffrey
Sent: Monday, March 10, 2003 1:26 PM
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Subject: U.S. Serial No. 09/191,772

88611

CF

Please search **SEQ ID NO.: 2** from the aforementioned application: **(09/191,772)** v. all relevant databases, including interference. Place results on both paper and disk. Thanks!

JSP
AU 1648
CM01-8E15
308-2227

Searcher: _____
Phone: _____
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Date Picked Up: _____
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Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
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Other (specify): _____

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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:44:28 ; Search time 30 Seconds
(without alignments)
103.024 Million cell updates/sec

Title: US-09-191-772A-2

Perfect score: 77

Sequence: 1 RIQGPGRFAFTIGK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL.21.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	35	15	Q76740 human immun
2	77	100.0	35	15	Q76741 human immun
3	77	100.0	35	15	Q79439 human immun
4	77	100.0	36	15	Q80545 human immun
5	77	100.0	36	15	Q80546 human immun
6	77	100.0	36	15	Q80547 human immun
7	77	100.0	36	15	Q80548 human immun
8	77	100.0	36	15	Q80549 human immun
9	77	100.0	36	15	Q80550 human immun
10	77	100.0	36	15	Q80551 human immun
11	77	100.0	36	15	Q79428 human immun
12	77	100.0	36	15	Q79429 human immun
13	77	100.0	36	15	Q79430 human immun
14	77	100.0	36	15	Q79433 human immun
15	77	100.0	36	15	Q79415 human immun
16	77	100.0	36	15	Q79416 human immun

17	77	100.0	36	15	Q79417 human immun
18	77	100.0	36	15	Q79418 human immun
19	77	100.0	36	15	Q79419 human immun
20	77	100.0	36	15	Q79434 human immun
21	77	100.0	36	15	Q79435 human immun
22	77	100.0	36	15	Q79437 human immun
23	77	100.0	36	15	Q79438 human immun
24	77	100.0	36	15	Q79536 human immun
25	77	100.0	36	15	Q79537 human immun
26	77	100.0	36	15	Q79539 human immun
27	77	100.0	36	15	Q79540 human immun
28	77	100.0	36	15	Q79542 human immun
29	77	100.0	36	15	Q79445 human immun
30	77	100.0	37	15	Q80552 human immun
31	77	100.0	41	15	Q77628 human immun
32	77	100.0	42	15	Q77622 human immun
33	77	100.0	42	15	Q77631 human immun
34	77	100.0	42	15	Q77660 human immun
35	77	100.0	42	15	Q77612 human immun
36	77	100.0	42	15	Q77665 human immun
37	77	100.0	42	15	Q77613 human immun
38	77	100.0	42	15	Q77623 human immun
39	77	100.0	42	15	Q77615 human immun
40	77	100.0	42	15	Q77614 human immun
41	77	100.0	45	15	Q97047 human immun
42	77	100.0	46	15	Q97055 human immun
43	77	100.0	55	15	O40263 human immun
44	77	100.0	56	15	O40267 human immun
45	77	100.0	57	15	Q97045 human immun

ALIGNMENTS

RESULT 1

ID Q76740 PRELIMINARY; PRT; 35 AA.
AC Q76740;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Env protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NO.5;
RX MEDLINE=96296970; PubMed=8679313;
RA Kakizawa J., Ushijima H., Morishita Y., Oka S., Ikeda Y., Muller W.E.;
RT "Diversity of HIV type 1 envelope V3 loop region in saliva."
RL AIDS Res. Hum. Retroviruses 12:561-563(1996).
DR EMBL; D78624; BA011444.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON TER 1
FT NON TER 35
SQ SEQUENCE 35 AA; 3950 MW; 48994EA4990F0279 CRC64;

Query Match 100.0%; Score 77; DB 15; Length 35;

Best Local Similarity 100.0%; Pred. No. 1.1e-06;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGPGRFAFTIGK 15

Db 13 RIQGPGRFAFTIGK 27

RESULT 2

ID Q76741 PRELIMINARY; PRT; 35 AA.

AC Q76741;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Env protein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NO.5;
 RX MEDLINE=96296970; PubMed=8679313;
 RA Kariyama J., Ushijima H., Morishita Y., Oka S., Ikeda Y., Muller W.E.;
 RT "Diversity of HIV type 1 envelope V3 loop region in saliva."
 RL AIDS Res. Hum. Retroviruses 12:561-563(1996).
 DR EMBL; D78625; BA01445.1; -.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 35
 SQ SEQUENCE 35 AA; 3950 MW; 48994EA4990F0279 CRC64;

 Query Match 100.0%; Score 77; DB 15; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 RIQGPGRFVTVIGK 15
 Db 13 RIQGPGRFVTVIGK 27

 RESULT 3
 ID Q79439 PRELIMINARY; PRT; 35 AA.
 AC Q79439;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Envelope protein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91240282; PubMed=2035026;
 RA Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
 RA Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
 RA Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
 RA Montagnier L.;
 RT "LAV revisited: Origins of the early viral HIV-1 isolates from
 RL Institut Pasteur."
 RL Science 252:961-965(1991).
 DR EMBL; M64207; AAA44765.1; -.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 35
 SQ SEQUENCE 35 AA; 3939 MW; A3DA68F9D10ADF1D CRC64;

 Query Match 100.0%; Score 77; DB 15; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 RIQGPGRFVTVIGK 15
 Db 12 RIQGPGRFVTVIGK 26

 RESULT 4
 ID Q80545 PRELIMINARY; PRT; 36 AA.
 AC Q80545;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Envelope protein (Fragment).

GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90364416; PubMed=2392685;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 RT neutralizing determinant."
 RL Science 249:932-935(1990).
 DR EMBL; M61582; AAA45268.1; -.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 36
 SQ SEQUENCE 36 AA; 4053 MW; 23A8994EA4990F02 CRC64;

 Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 RIQGPGRFVTVIGK 15
 Db 13 RIQGPGRFVTVIGK 27

 RESULT 5
 ID Q80546 PRELIMINARY; PRT; 36 AA.
 AC Q80546;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Envelope protein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90364416; PubMed=2392685;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 RT neutralizing determinant."
 RL Science 249:932-935(1990).
 DR EMBL; M61582; AAA45268.1; -.
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 36
 SQ SEQUENCE 36 AA; 4053 MW; 23A8994EA4990F02 CRC64;

 Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 RIQGPGRFVTVIGK 15
 Db 13 RIQGPGRFVTVIGK 27

 RESULT 6
 ID Q80547 PRELIMINARY; PRT; 36 AA.
 AC Q80547;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Envelope protein (Fragment).

Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQPGGRAFTVIGK 15
 DB 13 RIQPGGRAFTVIGK 27

RESULT 6

Q80547 ID Q80547 PRELIMINARY; PRT; 36 AA.
 AC Q80547;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE Envelope protein (Fragment).
 ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90364416; PubMed=2392685;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant.";
 RL Science 249:932-935(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91118022; PubMed=1990444;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant.";
 RL Science 251:811-811(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91361090; PubMed=1887238;
 RA LaRosa G.J., Weinhold K., Profy A.T., Langlois A.J., Dreesman G.R.,
 RA Boswell R.N., Shaddock P., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant: Further clarifications.";
 RL Science 253:1146-1146(1991).
 DR EMBL; M61586; AAA45270.1; -;
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 SQ SEQUENCE 36 AA; 4053 MW; 23A8994EA4990F02 CRC64;

Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQPGGRAFTVIGK 15
 DB 13 RIQPGGRAFTVIGK 27

RESULT 7

Q80548 ID Q80548 PRELIMINARY; PRT; 36 AA.
 AC Q80548;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE Envelope protein (Fragment).

GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90364416; PubMed=2392685;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant.";
 RL Science 249:932-935(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91118022; PubMed=1990444;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant: Corrections and clarifications.";
 RL Science 251:811-811(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91361090; PubMed=1887238;
 RA LaRosa G.J., Weinhold K., Profy A.T., Langlois A.J., Dreesman G.R.,
 RA Boswell R.N., Shaddock P., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant: Further clarifications.";
 RL Science 253:1146-1146(1991).
 DR EMBL; M61586; AAA45270.1; -;
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 SQ SEQUENCE 36 AA; 4053 MW; 23A8994EA4990F02 CRC64;

Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQPGGRAFTVIGK 15
 DB 13 RIQPGGRAFTVIGK 27

RESULT 8

Q80549 ID Q80549 PRELIMINARY; PRT; 36 AA.
 AC Q80549;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
 DE Envelope protein (Fragment).
 ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90364416; PubMed=2392685;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 neutralizing determinant.";
 RL Science 249:932-935(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91118022; PubMed=1990444;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,

QY 1 RIQPGGRAFTVIGK 15
 DB 13 RIQPGGRAFTVIGK 27

RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 RT neutralizing determinant: Corrections and clarifications.";
 RL Science 251:811-811(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91361090; PubMed=1887238;
 RA LaRosa G.J., Weinhold K., Profy A.T., Langlois A.J., Dreesman G.R.,
 RA Boswell R.N., Shaddock P., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 RT neutralizing determinant: Further clarifications.";
 RL Science 253:1146-1146(1991).
 DR EMBL; M61587; AAA45272.1; -;
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 SQ SEQUENCE 36 AA; 4122 MW; 23A9895FA4990F02 CRC64;
 Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQGPGRAPVTIGK 15
 Db 13 RIQGPGRAPVTIGK 27
 RESULT 9
 ID Q80550 PRELIMINARY; PRT; 36 AA.
 AC Q80550;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Envelope protein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90364416; PubMed=2392685;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 RT neutralizing determinant";
 RL Science 249:932-935(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90364416; PubMed=2392685;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 RT neutralizing determinant";
 RL Science 249:932-935(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91118022; PubMed=1990444;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 RT neutralizing determinant: Further clarifications.";
 RL Science 253:1146-1146(1991).
 DR EMBL; M61588; AAA45273.1; -;
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 SQ SEQUENCE 36 AA; 4193 MW; 62B118D6A4990F1E CRC64;
 Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQGPGRAPVTIGK 15
 Db 13 RIQGPGRAPVTIGK 27
 RESULT 11
 ID Q79428 PRELIMINARY; PRT; 36 AA.
 AC Q79428;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 FT NON_TER 1
 SQ SEQUENCE 36 AA; 4193 MW; 62B118D6A4990F1E CRC64;
 Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQGPGRAPVTIGK 15
 Db 13 RIQGPGRAPVTIGK 27

SQ SEQUENCE 36 AA; 4193 MW; 62B118D6A4990F1E CRC64;
 Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQGPGRAPVTIGK 15
 Db 13 RIQGPGRAPVTIGK 27
 RESULT 10
 ID Q80551 PRELIMINARY; PRT; 36 AA.
 AC Q80551;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Envelope protein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90364416; PubMed=2392685;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 RT neutralizing determinant";
 RL Science 249:932-935(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91118022; PubMed=1990444;
 RA LaRosa G.J., Davide J.P., Weinhold K., Waterbury J.A., Profy A.T.,
 RA Lewis J.A., Langlois A.J., Dreesman G.R., Boswell R.N., Shaddock P.,
 RA Holley L.H., Karplus M., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 RT neutralizing determinant: Corrections and clarifications.";
 RL Science 251:811-811(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91361090; PubMed=1887238;
 RA LaRosa G.J., Weinhold K., Profy A.T., Langlois A.J., Dreesman G.R.,
 RA Boswell R.N., Shaddock P., Bolognesi D.P., Matthews T.J., Emini E.A.,
 RA Putney S.D.;
 RT "Conserved sequence and structural elements in the HIV-1 principal
 RT neutralizing determinant: Further clarifications.";
 RL Science 253:1146-1146(1991).
 DR EMBL; M61589; AAA45274.1; -;
 KW AIDS; Coat protein; Glycoprotein.
 FT NON_TER 1
 SQ SEQUENCE 36 AA; 4193 MW; 62B118D6A4990F1E CRC64;
 Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQGPGRAPVTIGK 15
 Db 13 RIQGPGRAPVTIGK 27
 RESULT 11
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 AC Q79428;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 FT NON_TER 1
 SQ SEQUENCE 36 AA; 4193 MW; 62B118D6A4990F1E CRC64;
 Query Match 100.0%; Score 77; DB 15; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQGPGRAPVTIGK 15
 Db 13 RIQGPGRAPVTIGK 27

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DE Envelope protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91240282; PubMed=2035026;
RA Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA Montagnier L.;
RT "LAV revisited: Origins of the early viral HIV-1 isolates from
RT Institut Pasteur.";
RL Science 252:961-965(1991).
DR EMBL; M64187; AAA44755.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 36 AA; 4053 MW; 23A8994EA4990F02 CRC64;

Query Match 100.0%; Score 77; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGFAFVTIGK 15
DB 13 RIQGGGFAFVTIGK 27

RESULT 12
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DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Envelope protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91240282; PubMed=2035026;
RA Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA Montagnier L.;
RT "LAV revisited: Origins of the early viral HIV-1 isolates from
RT Institut Pasteur.";
RL Science 252:961-965(1991).
DR EMBL; M64187; AAA44755.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 36 AA; 4053 MW; 23A8994EA4990F02 CRC64;

Query Match 100.0%; Score 77; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGFAFVTIGK 15
DB 13 RIQGGGFAFVTIGK 27

RESULT 13
Q79430 ID Q79430 PRELIMINARY; PRT; 36 AA.
AC Q79430;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Envelope protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91240282; PubMed=2035026;
RA Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA Montagnier L.;
RT "LAV revisited: Origins of the early viral HIV-1 isolates from
RT Institut Pasteur.";
RL Science 252:961-965(1991).
DR EMBL; M64187; AAA44755.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 36 AA; 4053 MW; 23A8994EA4990F02 CRC64;

Query Match 100.0%; Score 77; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGFAFVTIGK 15
DB 13 RIQGGGFAFVTIGK 27

RESULT 14
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AC Q79433;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Envelope protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91240282; PubMed=2035026;
RA Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA Montagnier L.;
RT "LAV revisited: Origins of the early viral HIV-1 isolates from
RT Institut Pasteur.";
RL Science 252:961-965(1991).
DR EMBL; M64190; AAA44759.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 36 AA; 4053 MW; 23A8994EA4990F02 CRC64;

Query Match 100.0%; Score 77; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGFAFVTIGK 15
DB 13 RIQGGGFAFVTIGK 27

RESULT 15
Q79415 ID Q79415 PRELIMINARY; PRT; 36 AA.
AC Q79415;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Envelope protein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91240282; PubMed=2035026;
RA Wain-Hobson S., Vartanian J.-P., Henry M., Chenciner N., Cheynier R.,
RA Delassus S., Martins L.P., Sala M., Nugeyre M.-T., Guetard D.,
RA Klatzmann D., Gluckman J.-C., Rozenbaum W., Barre-Sinoussi F.,
RA Montagnier L.;
RT "LAV revisited: Origins of the early viral HIV-1 isolates from
RT Institut Pasteur.";
RL Science 252:961-965(1991).
DR EMBL; M64190; AAA44759.1; -.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 36 AA; 4053 MW; 23A8994EA4990F02 CRC64;

Query Match 100.0%; Score 77; DB 15; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGFAFVTIGK 15
DB 13 RIQGGGFAFVTIGK 27
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FT CARBOHYD 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 443 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 632 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 669 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 811 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 851 AA; 96644 MW; D16A3C90857785F1 CRC64;
 Query Match 100.0%; Score 77; DB 1; Length 851;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQGFGRFVTVIGK 15
 DQ 308 RIQGFGRFVTVIGK 322
 RESULT 2
 ENV_HVIMF STANDARD; PRT; 853 AA.
 AC P19551;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 GN ENV.
 OS Human immunodeficiency virus type 1 (MFA isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11704;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90317877; PubMed=1695254;
 RA Stevenson M., Haggerty S., Lamonic C., Mann A.M., Meier C., Wasia A.;
 RA "Cloning and characterization of human immunodeficiency virus type 1 variants diminished in the ability to induce syncytium-independent cytolysis.";
 RT J. Virol. 64:3792-3803(1990).
 RL
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 CC -----
 DR EMBL; M33943; AAA44850.1; -;
 DR HIV; M33943; ENV\$MFA.
 DR InterPro; IPR000328; ENV GP41.
 DR InterPro; IPR000777; GP120.
 DR Pfam; PF00516; GP120; 1.
 DR

DR Pfam; PF00517; GP41; 1.
 KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 509
 FT CHAIN 510 853
 FT DISULFID 54 74
 FT DISULFID 119 203
 FT DISULFID 126 194
 FT DISULFID 131 157
 FT DISULFID 216 245
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 FT DISULFID 294 329
 FT DISULFID 376 443
 FT DISULFID 383 416
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 FT CARBOHYD 136 136
 FT CARBOHYD 141 141
 FT CARBOHYD 156 156
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 FT CARBOHYD 186 186
 FT CARBOHYD 195 195
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 FT CARBOHYD 672 672
 FT CARBOHYD 748 748
 FT CARBOHYD 814 814
 SQ SEQUENCE 853 AA; 96912 MW; 3377B993B6F22ABA CRC64;
 Query Match 100.0%; Score 77; DB 1; Length 853;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQGFGRFVTVIGK 15
 DQ 306 RIQGFGRFVTVIGK 320
 RESULT 3
 ENV_HVIB1 STANDARD; PRT; 856 AA.
 AC P03375;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Envelope glycoprotein GP160 precursor (Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
 GN ENV.
 OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11678;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8511123; PubMed=2578615;
 RA Ratner L., Haeeltine W., Patarca R., Livak K.J., Starcich B.R., Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,

FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 156 156 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 197 197 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 230 230 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 234 234 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 241 241 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97212 MW; 6FAB16AF85107FE0 CRC64;

Query Match 100.0%; Score 77; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 4e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 RIQGRGPAFTVIGK 15
DB 308 RIQGRGPAFTVIGK 322

RESULT 5
ENV HV1H3 STANDARD; PRT; 856 AA.
ID P04624;
AC 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HXB3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11707;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85228248; PubMed=2988795;
RA Crowl R., Ganguly K., Gordon M., Conroy R., Schaber M., Kramer R., Shaw G.M., Wong-Staal F., Reddy E.P.;
RT "HTLV-III env gene products synthesized in E. coli are recognized by antibodies present in the sera of AIDS patients.";
RL Cell 41:979-986(1985).
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CC -----
CC EMBL; M14100; AAA44679.1; -;
DR HIV; M14100; ENV\$HXB3.
DR InterPro; IPR000328; Env_GP41.

DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.
KW SIGNAL. 1 30
FT CHAIN 31 511 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 512 856 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 119 205 BY SIMILARITY.
FT DISULFID 126 196 BY SIMILARITY.
FT DISULFID 131 157 BY SIMILARITY.
FT DISULFID 218 247 BY SIMILARITY.
FT DISULFID 228 239 BY SIMILARITY.
FT DISULFID 296 331 BY SIMILARITY.
FT DISULFID 378 445 BY SIMILARITY.
FT DISULFID 385 418 BY SIMILARITY.
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FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 262 262 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 301 301 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 339 339 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. .) (POTENTIAL).
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FT CARBOHYD 392 392 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 397 397 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 448 448 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 463 463 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 611 611 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 637 637 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 674 674 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 750 750 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 816 816 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 856 AA; 97188 MW; 3373C68B84C1AFC CRC64;

Query Match 100.0%; Score 77; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 4e-06; Indels 0; Gaps 0;
Matches 15; Conservative 0; Mismatches 0;

QY 1 RIQGRGPAFTVIGK 15
DB 308 RIQGRGPAFTVIGK 322

RESULT 6
ENV HV1PV STANDARD; PRT; 856 AA.
ID ENV HV1PV
AC P03376;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11700;
RN [1]
RP SEQUENCE FROM N.A.


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FT CARBOHYD 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT CARBOHYD 391 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 411 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 468 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 621 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 630 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 642 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 679 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 755 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 821 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 861 AA; 97487 MW; 04DE2B4D4E4FD63A CRC64;

Query Match 100.0%; Score 77; DB 1; Length 861;
Best Local Similarity 100.0%; Pred. No. 4e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIORGPGRAFVTIGK 15
DB 313 RIORGPGRAFVTIGK 327
|||||

RESULT 8
ENV_HVILW STANDARD; PRT; 856 AA.
ID AC Q70626;
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HIV type 11IB)";
RL AIDS Res. Hum. Retroviruses 10:1143-1155(1994).
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CC -----
CC ENBL; U12055; AAA76690.1; --
CC GlycoSuiteDB; Q70626; --
CC InterPro; IPR000328; Env GP41.
CC InterPro; IPR000777; GP120.
CC Pfam; PF00516; GP120; 1.
CC Pfam; PF00517; GP41; 1.
CC AIDS; Coat protein; Glycoprotein; Transmembrane;
CC Signal.
CC CHAIN 1 30
CC CHAIN 31 511
CC CHAIN 512 856
CC DISULFID 54 74
CC DISULFID 119 205
CC DISULFID 126 196
CC DISULFID 131 157
CC DISULFID 218 247
CC DISULFID 228 239
CC BY SIMILARITY.
CC EXTERIOR MEMBRANE GLYCOPROTEIN.
CC TRANSMEMBRANE GLYCOPROTEIN.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.
CC BY SIMILARITY.

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FT DISULFID 296 BY SIMILARITY.
FT DISULFID 378 BY SIMILARITY.
FT DISULFID 385 BY SIMILARITY.
FT CARBOHYD 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 197 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 241 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 289 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 301 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 397 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 463 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 611 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 624 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 637 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 674 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 750 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 816 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 856 AA; 96938 MW; 0C241332CF7B5687 CRC64;

Query Match 94.8%; Score 73; DB 1; Length 856;
Best Local Similarity 93.3%; Pred. No. 2.1e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RIORGPGRAFVTIGK 15
DB 308 RIORGPGRAFVTIGK 322
|||||

RESULT 9
ENV_HVILJ STANDARD; PRT; 848 AA.
ID AC P20871;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11688;
RN [1]
RP SEQUENCE FROM N.A.
RA Koyanagi S., Chen I.S.Y.;
RL Submitted (DEC-1988) to the HIV data bank.
CC -----
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CC -----
CC ENBL; M38429; AAB03749.1; --
CC HIV; M38429; ENVJRCSF.

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FT DISULFID 388 457 BY SIMILARITY.
FT CARBOHYD 395 430 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 867 AA; 98399 MW; 5F2310146B8E8680 CRC64;

Query Match 57.1%; Score 44; DB 1; Length 867;
Best Local Similarity 75.0%; Pred. No. 3.9; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

-Qy. 1 RIQGFGRFVFT 12
    || |||||
Db 318 RHIGGRAFT 329

-RESULT 13
ENV HV1A2
ID ENV HV1A2 STANDARD; PRT; 855 AA.
AC P03378;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (ARV2/SP2 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85090453; PubMed=2578227;
RA Sanchez-Pescador R., Power M.D., Barr P.J., Steimer K.S.,
RA Stempien M.M., Brown-Shimer S.L., Gee W.W., Renard A., Randolph A.,
RA Levy J.A., Dina D., Luciw P.A.;
RT "Nucleotide sequence and expression of an AIDS-associated retrovirus
RT (ARV-2)".
RL Science 227:484-492 (1985).
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CC EMBL; K02007; AAB59882.1; -.
DR PIR; A03976; VCLJAJ2.
DR HIV; K02007; ENVSSF2.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane;
KW SIGNAL.
FT CHAIN 1 29
FT CHAIN 30 509 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 510 855 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 208 BY SIMILARITY.
FT DISULFID 125 199 BY SIMILARITY.
FT DISULFID 130 155 BY SIMILARITY.
FT DISULFID 221 250 BY SIMILARITY.
FT DISULFID 231 242 BY SIMILARITY.
FT DISULFID 299 333 BY SIMILARITY.
FT DISULFID 380 442 BY SIMILARITY.
FT DISULFID 387 415 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 298 298 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 304 304 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 341 341 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 358 358 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 364 364 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 394 394 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 461 461 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 610 610 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 624 624 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 815 815 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 855 AA; 97438 MW; A3BC20573AAC41A2 CRC64;

Query Match 55.8%; Score 43; DB 1; Length 855;
Best Local Similarity 72.7%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GPGRAFTVIGK 15
    |||||
Db 313 GPGRAFTTGR 323

RESULT 14
ENV HV1KB
ID ENV HV1KB STANDARD; PRT; 861 AA.
AC P31819;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polyprotein GP160 precursor [Contains: Exterior membrane
DE glycoprotein (GP120); Transmembrane glycoprotein (GP41)].

```


Query Match 55.8%; Score 43; DB 1; Length 1236;
Best Local Similarity 42.9%; Pred. NO. 8.5;
Matches 6; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 2 LQGGGGRAFVTIGK 15
::||| |::||
Db 873 VRRGPDNEFIAGK 886

Search completed: March 10, 2003, 17:51:36
Job time : 12 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:45:18 ; Search time 21 Seconds
(without alignments)
68.667 Million cell updates/sec

Title: US-09-191-772A-2

Perfect score: 77

Sequence: 1 RIQRGGRAFTVIGK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:*

1: Pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	100.0	851	2 S33985	env polyprotein -
2	77	100.0	854	2 S13288	env protein - huma
3	77	100.0	856	1 VCLJH3	env polyprotein pr
4	77	100.0	856	1 VCLJVL	env polyprotein pr
5	77	100.0	861	1 VCLJLV	env polyprotein pr
6	60	77.9	20	2 S65399	immunodeficiency v
7	52	67.5	861	1 VCLJSC	env polyprotein pr
8	47	61.0	35	2 PC2296	V3 domain peptide
9	45	58.4	35	2 PC2295	env domain peptide
10	45	58.4	77	2 S35809	env protein -
11	45	58.4	77	2 S35808	env protein -
12	45	58.4	77	2 S35848	env protein -
13	45	58.4	77	2 S35815	env protein -
14	45	58.4	77	2 S35849	env protein -
15	45	58.4	77	2 S35861	env protein -
16	45	58.4	77	2 S35862	env protein -
17	45	58.4	110	2 A46410	env protein (
18	45	58.4	110	2 D46410	env protein (
19	45	58.4	443	2 C41621	env polyprotein p
20	45	58.4	685	2 B82606	conjugal transfer
21	45	58.4	847	2 T09448	env envelope glycoprot
22	45	58.4	847	2 S13289	env protein - huma
23	44	57.1	77	2 S35807	env protein -
24	44	57.1	77	2 S35816	env protein -
25	44	57.1	445	2 A41621	env polyprotein M
26	44	57.1	454	2 B41621	env polyprotein D
27	44	57.1	687	2 T08528	probable DNA topoi
28	44	57.1	852	1 VCLJBR	env polyprotein -
29	44	57.1	859	1 VCLJMN	env polyprotein pr

30 43 55.8 76 2 S35859 envelope protein -
31 43 55.8 77 2 S35858 envelope protein -
32 43 55.8 77 2 S35821 envelope protein -
33 43 55.8 77 2 S35857 envelope protein -
34 43 55.8 77 2 S35819 envelope protein -
35 43 55.8 77 2 S35820 envelope protein -
36 43 55.8 729 1 VCLJTX env polyprotein pr
37 43 55.8 812 2 T48016 probable zinc-fing
38 43 55.8 855 1 VCLJAJ env polyprotein pr
39 43 55.8 861 1 VCLJKB env polyprotein pr
40 42 54.5 71 2 S42918 env polyprotein -
41 42 54.5 316 2 H90372 catechol 2,3-dioxy
42 41 53.2 71 2 S42904 env polyprotein -
43 41 53.2 71 2 S42905 env polyprotein -
44 41 53.2 77 2 S35835 envelope protein -
45 41 53.2 77 2 S35836 envelope protein -

ALIGNMENTS

RESULT 1

S33985

env polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F.

submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:Z11530; NID:G60192; PIDN:CAA77628.1; PID:G60199

C:Superfamily: type E retrovirus env polyprotein

Query Match

Best Local Similarity 100.0%; Score 77; DB 2; Length 851;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQRGGRAFTVIGK 15

DB 308 RIQRGGRAFTVIGK 322

RESULT 2

S13288

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S13288

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Digne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120 c

A:Reference number: S13288; MUID:91043044; PMID:2172833

A:Accession: S13288

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-854 <OBR>

C:Superfamily: type E retrovirus env polyprotein

Query Match

Best Local Similarity 100.0%; Score 77; DB 2; Length 854;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQRGGRAFTVIGK 15

DB 306 RIQRGGRAFTVIGK 320

RESULT 3

VCLJH3

C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03975
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03975
A;Molecule type: DNA
A;Residues: 1-861 <WAI>
A;Cross-references: GB:R02013; NID:G326417; PIDN:AAB59751.1; PID:G326424
C;Genetics:
C;Gene: env
C;Superfamily: type E retrovirus env polyprotein
C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-516/Product: exterior membrane glycoprotein #status predicted <EXT>
F;517-861/Product: transmembrane glycoprotein #status predicted <TM>
F;88,136,141,146,161,165,191,202,239,246,267,281,294,300,306,337,344,361,391,397,402,411,417,421,425,429,432,435,438,441,444,447,450,453,456,459,462,465,468,471,474,477,480,483,486,489,492,495,498,501,504,507,510,513,516,519,522,525,528,531,534,537,540,543,546,549,552,555,558,561,564,567,570,573,576,579,582,585,588,591,594,597,600,603,606,609,612,615,618,621,624,627,630,633,636,639,642,645,648,651,654,657,660,663,666,669,672,675,678,681,684,687,690,693,696,699,702,705,708,711,714,717,720,723,726,729,732,735,738,741,744,747,750,753,756,759,762,765,768,771,774,777,780,783,786,789,792,795,798,801,804,807,810,813,816,819,822,825,828,831,834,837,840,843,846,849,852,855,858,861,864,867,870,873,876,879,882,885,888,891,894,897,899,902,905,908,911,914,917,920,923,926,929,932,935,938,941,944,947,950,953,956,959,962,965,968,971,974,977,980,983,986,989,992,995,998,1001,1004,1007,1010,1013,1016,1019,1022,1025,1028,1031,1034,1037,1040,1043,1046,1049,1052,1055,1058,1061,1064,1067,1070,1073,1076,1079,1082,1085,1088,1091,1094,1097,1100,1103,1106,1109,1112,1115,1118,1121,1124,1127,1130,1133,1136,1139,1142,1145,1148,1151,1154,1157,1160,1163,1166,1169,1172,1175,1178,1181,1184,1187,1190,1193,1196,1199,1202,1205,1208,1211,1214,1217,1220,1223,1226,1229,1232,1235,1238,1241,1244,1247,1250,1253,1256,1259,1262,1265,1268,1271,1274,1277,1280,1283,1286,1289,1292,1295,1298,1301,1304,1307,1310,1313,1316,1319,1322,1325,1328,1331,1334,1337,1340,1343,1346,1349,1352,1355,1358,1361,1364,1367,1370,1373,1376,1379,1382,1385,1388,1391,1394,1397,1400,1403,1406,1409,1412,1415,1418,1421,1424,1427,1430,1433,1436,1439,1442,1445,1448,1451,1454,1457,1460,1463,1466,1469,1472,1475,1478,1481,1484,1487,1490,1493,1496,1499,1502,1505,1508,1511,1514,1517,1520,1523,1526,1529,1532,1535,1538,1541,1544,1547,1550,1553,1556,1559,1562,1565,1568,1571,1574,1577,1580,1583,1586,1589,1592,1595,1598,1601,1604,1607,1610,1613,1616,1619,1622,1625,1628,1631,1634,1637,1640,1643,1646,1649,1652,1655,1658,1661,1664,1667,1670,1673,1676,1679,1682,1685,1688,1691,1694,1697,1700,1703,1706,1709,1712,1715,1718,1721,1724,1727,1730,1733,1736,1739,1742,1745,1748,1751,1754,1757,1760,1763,1766,1769,1772,1775,1778,1781,1784,1787,1790,1793,1796,1799,1802,1805,1808,1811,1814,1817,1820,1823,1826,1829,1832,1835,1838,1841,1844,1847,1850,1853,1856,1859,1862,1865,1868,1871,1874,1877,1880,1883,1886,1889,1892,1895,1898,1901,1904,1907,1910,1913,1916,1919,1922,1925,1928,1931,1934,1937,1940,1943,1946,1949,1952,1955,1958,1961,1964,1967,1970,1973,1976,1979,1982,1985,1988,1991,1994,1997,1999,2002,2005,2008,2011,2014,2017,2020,2023,2026,2029,2032,2035,2038,2041,2044,2047,2050,2053,2056,2059,2062,2065,2068,2071,2074,2077,2080,2083,2086,2089,2092,2095,2098,2101,2104,2107,2110,2113,2116,2119,2122,2125,2128,2131,2134,2137,2140,2143,2146,2149,2152,2155,2158,2161,2164,2167,2170,2173,2176,2179,2182,2185,2188,2191,2194,2197,2200,2203,2206,2209,2212,2215,2218,2221,2224,2227,2230,2233,2236,2239,2242,2245,2248,2251,2254,2257,2260,2263,2266,2269,2272,2275,2278,2281,2284,2287,2290,2293,2296,2299,2302,2305,2308,2311,2314,2317,2320,2323,2326,2329,2332,2335,2338,2341,2344,2347,2350,2353,2356,2359,2362,2365,2368,2371,2374,2377,2380,2383,2386,2389,2392,2395,2398,2401,2404,2407,2410,2413,2416,2419,2422,2425,2428,2431,2434,2437,2440,2443,2446,2449,2452,2455,2458,2461,2464,2467,2470,2473,2476,2479,2482,2485,2488,2491,2494,2497,2500,2503,2506,2509,2512,2515,2518,2521,2524,2527,2530,2533,2536,2539,2542,2545,2548,2551,2554,2557,2560,2563,2566,2569,2572,2575,2578,2581,2584,2587,2590,2593,2596,2599,2602,2605,2608,2611,2614,2617,2620,2623,2626,2629,2632,2635,2638,2641,2644,2647,2650,2653,2656,2659,2662,2665,2668,2671,2674,2677,2680,2683,2686,2689,2692,

A:Gene: env
 C:Superfamily: type E retrovirus env polypotein
 C:Keywords: capsid protein; coat protein; glycoprotein; polypotein; transmembrane prote
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-861/Product: env polypotein #status predicted <EPP>
 F:87,129,135,140,143,159,163,187,198,234,241,262,276,295,301,302,333,340,356,362,386,396

Query Match 67.5%; Score 52; DB 1; Length 861;
 Best Local Similarity 76.9%; Pred. No. 0.58;
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 IORGPGRAFTVIG 14
 |||||
 Db 309 IORGPGRAFTYATG 321

RESULT 8
 PC2296
 V3 domain peptide P4346 - human immunodeficiency virus type 1 (fragment)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 07-May-1999
 C:Accession: PC2296
 R;Sherafa, K.; Soennerborg, A.; Steinbergs, J.; Saelberg, M.
 Biochem. Biophys. Res. Commun. 205: 1658-1664, 1994
 A>Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping a
 A:Reference number: PC2291; PMID:95110306; PMID:7811250
 A:Accession: PC2296
 A:Molecule type: protein
 A:Residues: 1-35 <SHE>
 C:Superfamily: type E retrovirus env polypotein

Query Match 61.0%; Score 47; DB 2; Length 35;
 Best Local Similarity 64.3%; Pred. No. 0.22;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IORGPGRAFTVIG 15
 |||||
 Db 12 IHMGPGRAFTTGE 25

RESULT 9
 PC2295
 V3 domain peptide P4317 - human immunodeficiency virus type 1 (fragment)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 07-May-1999
 C:Accession: PC2295
 R;Sherafa, K.; Soennerborg, A.; Steinbergs, J.; Saelberg, M.
 Biochem. Biophys. Res. Commun. 205: 1658-1664, 1994
 A>Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping a
 A:Reference number: PC2291; PMID:95110306; PMID:7811250
 A:Accession: PC2295
 A:Molecule type: protein
 A:Residues: 1-35 <SHE>
 C:Superfamily: type E retrovirus env polypotein

Query Match 58.4%; Score 45; DB 2; Length 35;
 Best Local Similarity 64.3%; Pred. No. 0.49;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IORGPGRAFTVIG 15
 |||||
 Db 12 IHMGPGRAFTTGE 25

RESULT 10
 S35809
 envelope protein - human immunodeficiency virus type 1 (fragment)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S35809
 R;Chiodi, F.
 submitted to the EMBL Data Library, June 1993
 A:Reference number: S35800

A:Accession: S35809
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 <CHI>
 A:Cross-references: EMBL:Z23187; NID:G313523; PIDN:CAA80708.1; PID:G313524
 C:Superfamily: type E retrovirus env polypotein

Query Match 58.4%; Score 45; DB 2; Length 77;
 Best Local Similarity 64.3%; Pred. No. 1;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IORGPGRAFTVIG 15
 |||||
 Db 37 IHIGPGRAFTTGG 50

RESULT 11
 S35808
 envelope protein - human immunodeficiency virus type 1 (fragment)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S35808
 R;Chiodi, F.
 submitted to the EMBL Data Library, June 1993
 A:Reference number: S35800
 A:Accession: S35808
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 <CHI>
 A:Cross-references: EMBL:Z23186; NID:G313521; PIDN:CAA80707.1; PID:G313522
 C:Superfamily: type E retrovirus env polypotein

Query Match 58.4%; Score 45; DB 2; Length 77;
 Best Local Similarity 64.3%; Pred. No. 1;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IORGPGRAFTVIG 15
 |||||
 Db 37 IHIGPGRAFTTGG 50

RESULT 12
 S35848
 envelope protein - human immunodeficiency virus type 1 (fragment)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S35848
 R;Chiodi, F.
 submitted to the EMBL Data Library, June 1993
 A:Reference number: S35800
 A:Accession: S35848
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 <CHI>
 A:Cross-references: EMBL:Z23232; NID:G313607; PIDN:CAA80750.1; PID:G313608
 C:Superfamily: type E retrovirus env polypotein

Query Match 58.4%; Score 45; DB 2; Length 77;
 Best Local Similarity 64.3%; Pred. No. 1;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IORGPGRAFTVIG 15
 |||||
 Db 37 IHIGPGRAFTTGG 50

RESULT 13
 S35815
 envelope protein - human immunodeficiency virus type 1 (fragment)
 C:Species: human immunodeficiency virus type 1, HIV-1
 C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 26-Aug-1999
 C:Accession: S35815
 R;Chiodi, F.
 submitted to the EMBL Data Library, June 1993
 A:Reference number: S35800

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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:52:24 ; Search time 15 Seconds
(without alignments)
42.170 Million cell updates/sec

Title: US-09-191-772A-2

Perfect score: 77

Sequence: 1 RIORGPGRAFTVIGK 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188354 seqs, 42170167 residues

Total number of hits satisfying chosen parameters: 188354

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	15	10	US-09-810-310-15
2	77	100.0	15	10	US-09-810-310-24
3	77	100.0	15	10	US-09-886-621-8
4	77	100.0	20	10	US-09-813-659-3
5	77	100.0	26	10	US-09-889-621-9
6	77	100.0	30	10	US-09-810-310-6
7	77	100.0	31	10	US-09-810-310-7
8	77	100.0	35	10	US-09-810-310-1
9	77	100.0	36	9	US-09-886-156-66
10	77	100.0	36	9	US-09-886-150-66
11	77	100.0	36	9	US-10-012-507-4
12	77	100.0	36	9	US-09-886-149-66
13	77	100.0	36	9	US-09-886-159-66
14	77	100.0	39	10	US-09-810-310-2
15	77	100.0	39	10	US-09-810-310-3
16	77	100.0	42	10	US-09-810-310-5
17	77	100.0	48	10	US-09-810-310-4
18	77	100.0	511	10	US-09-796-202-17
19	77	100.0	519	10	US-09-756-551A-8

20	77	100.0	853	9	US-10-003-035-33	Sequence 33, Appl
21	77	100.0	856	10	US-09-476-242-1	Sequence 1, Appl
22	77	100.0	1101	9	US-10-003-035-53	Sequence 53, Appl
23	77	100.0	1186	9	US-10-003-035-55	Sequence 55, Appl
24	66	85.7	41	9	US-09-956-940-22	Sequence 22, Appl
25	66	85.7	41	9	US-09-956-940-25	Sequence 25, Appl
26	66	85.7	53	9	US-09-956-940-23	Sequence 23, Appl
27	62	80.5	20	9	US-09-827-345-24	Sequence 24, Appl
28	58	75.3	15	10	US-09-901-106-10	Sequence 10, Appl
29	57	74.0	17	10	US-09-901-106-12	Sequence 12, Appl
30	52	67.5	10	9	US-09-087-513-7	Sequence 7, Appl
31	52	67.5	10	9	US-09-087-513-13	Sequence 13, Appl
32	52	67.5	10	9	US-10-113-085-7	Sequence 7, Appl
33	52	67.5	10	9	US-09-997-848A-16	Sequence 16, Appl
34	52	67.5	10	10	US-09-858-349-3	Sequence 3, Appl
35	52	67.5	10	10	US-09-810-310-16	Sequence 16, Appl
36	52	67.5	10	10	US-09-820-484-8	Sequence 8, Appl
37	48	62.3	9	9	US-09-997-848A-1	Sequence 1, Appl
38	45	58.4	19	10	US-09-308-511-1	Sequence 1, Appl
39	45	58.4	376	9	US-09-934-060A-28	Sequence 28, Appl
40	45	58.4	502	10	US-09-796-202-16	Sequence 16, Appl
41	45	58.4	506	9	US-09-934-060A-24	Sequence 24, Appl
42	45	58.4	506	9	US-09-934-060A-30	Sequence 30, Appl
43	45	58.4	556	9	US-09-934-060A-6	Sequence 6, Appl
44	45	58.4	590	9	US-09-934-060A-13	Sequence 13, Appl
45	45	58.4	720	9	US-09-934-060A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-810-310-15
; Sequence 15, Application US/09810310
; Patent No. US2002004948A1
; GENERAL INFORMATION: Samir N.
; APPLICANT: Khleif, Samir N.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-15

Query Match 100.0%; Score 77; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIORGPGRAFTVIGK 15
Db 1 RIORGPGRAFTVIGK 15

RESULT 2
US-09-810-310-24
; Sequence 24, Application US/09810310
; Patent No. US2002004948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF

; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
 ; FILE REFERENCE: 15280-415100US
 ; CURRENT APPLICATION NUMBER: US/09/810,310
 ; CURRENT FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/189,396
 ; PRIOR FILING DATE: 2000-03-15
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
 ; OTHER INFORMATION: ANTIGEN
 ; US-09-810-310-24

Query Match 100.0%; Score 77; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.6e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGPGRFVTVIGK 15
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 Db 1 RIQGPGRFVTVIGK 15

RESULT 3

US-09-989-621-8
 ; Sequence 8, Application US/09989621
 ; Patent No. US20020151683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mogam Biotechnology Research Institute
 ; APPLICANT: Kim, Tae-Young
 ; APPLICANT: Lee, Ki-Young
 ; APPLICANT: Chang, Jin-Soo
 ; APPLICANT: Cho, Sung-Yoo
 ; APPLICANT: Hwang, Yu-Kyeong
 ; APPLICANT: Choi, Myeong
 ; APPLICANT: Cheong, Hong-Seok
 ; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
 ; FILE REFERENCE: 0136/OE154
 ; CURRENT APPLICATION NUMBER: US/09/989,621
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 09/051,006
 ; PRIOR FILING DATE: 2000-11-17
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 8
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: HIV
 ; US-09-989-621-8

Query Match 100.0%; Score 77; DB 10; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.6e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGPGRFVTVIGK 15
 |||||
 Db 1 RIQGPGRFVTVIGK 15

RESULT 4

US-09-813-659-3
 ; Sequence 3, Application US/09813659
 ; Patent No. US20020012989A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Hayden, Martha S.
 ; APPLICANT: Linsley, Peter S.
 ; APPLICANT: Bajorath, Jurgen
 ; APPLICANT: Fell, H. Perry

; APPLICANT: Gilliland, Lisa K.
 ; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING BISPECIFIC FUSION PROTEINS
 ; TITLE OF INVENTION: AND METHODS OF PRODUCING BIOLOGICALLY ACTIVE BISPECIFIC
 ; TITLE OF INVENTION: FUSION PROTEINS IN A MAMMALIAN CELL
 ; FILE REFERENCE: 30436.18USD2
 ; CURRENT APPLICATION NUMBER: US/09/813,659
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 09/549,067
 ; PRIOR FILING DATE: 2000-04-13
 ; PRIOR APPLICATION NUMBER: 08/539,436
 ; PRIOR FILING DATE: 1995-10-05
 ; PRIOR APPLICATION NUMBER: 08/121,054
 ; PRIOR FILING DATE: 1993-09-13
 ; PRIOR APPLICATION NUMBER: 08/013,420
 ; PRIOR FILING DATE: 1993-02-01
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-813-659-3

Query Match 100.0%; Score 77; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGPGRFVTVIGK 15
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 Db 5 RIQGPGRFVTVIGK 19

RESULT 5

US-09-989-621-9
 ; Sequence 9, Application US/09989621
 ; Patent No. US20020151683A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mogam Biotechnology Research Institute
 ; APPLICANT: Kim, Tae-Young
 ; APPLICANT: Lee, Ki-Young
 ; APPLICANT: Chang, Jin-Soo
 ; APPLICANT: Cho, Sung-Yoo
 ; APPLICANT: Hwang, Yu-Kyeong
 ; APPLICANT: Choi, Myeong
 ; APPLICANT: Cheong, Hong-Seok
 ; TITLE OF INVENTION: Liposomes Comprising Peptide Antigens
 ; FILE REFERENCE: 0136/OE154
 ; CURRENT APPLICATION NUMBER: US/09/989,621
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 09/051,006
 ; PRIOR FILING DATE: 2000-11-17
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 9
 ; LENGTH: 26
 ; TYPE: PRT
 ; ORGANISM: HIV
 ; US-09-989-621-9

Query Match 100.0%; Score 77; DB 10; Length 26;
 Best Local Similarity 100.0%; Pred. No. 1.4e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGPGRFVTVIGK 15
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 Db 12 RIQGPGRFVTVIGK 26

RESULT 6

US-09-810-310-6
 ; Sequence 6, Application US/09810310
 ; Patent No. US20020044948A1

; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-6

Query Match 100.0%; Score 77; DB 10; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQGGGGRFVTVIGK 15
Db 16 RIQGGGGRFVTVIGK 30
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RESULT 7
US-09-810-310-7
; Sequence 7, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-7

Query Match 100.0%; Score 77; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQGGGGRFVTVIGK 15
Db 17 RIQGGGGRFVTVIGK 31
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RESULT 8
US-09-810-310-1
; Sequence 1, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Berzofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS

; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-1

Query Match 100.0%; Score 77; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQGGGGRFVTVIGK 15
Db 21 RIQGGGGRFVTVIGK 35
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RESULT 9
US-09-886-156-66
; Sequence 66, Application US/09886156
; Patent No. US2002015428A1
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 03495-0001-04
; CURRENT APPLICATION NUMBER: US/09/886,156
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US/09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-886-156-66

Query Match 100.0%; Score 77; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQGGGGRFVTVIGK 15
Db 13 RIQGGGGRFVTVIGK 27
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RESULT 10
US-09-886-150-66
; Sequence 66, Application US/09886150
; Patent No. US20020172939A1
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef

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; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495.0001-04
; CURRENT APPLICATION NUMBER: US/09/886,150
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-886-150-66

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Query Match 100.0%; Score 77; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 RIQGGGFAVTVIGK 15
Db 13 RIQGGGFAVTVIGK 27

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RESULT 11
US-10-012-507-4
; Sequence 4, Application US/10012507
; Patent No. US20020173446A1
; GENERAL INFORMATION:
; APPLICANT: Kwong, Peter
; APPLICANT: Hendrickson, Wayne
; APPLICANT: Wyatt, Richard
; APPLICANT: Sodroski, Joseph
; TITLE OF INVENTION: COMPOUNDS WHICH BIND TO THE CENTRAL CAVITY BETWEEN HIV-1 gp120 AND
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 0575/63618-A
; CURRENT APPLICATION NUMBER: US/10/012,507
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 36
; TYPE: PRT
; ORGANISM: HXBc2 (a laboratory - adapted HIV-1 isolate)
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(36)
; OTHER INFORMATION: V3 loop of gp120 core
US-10-012-507-4

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Query Match 100.0%; Score 77; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 RIQGGGFAVTVIGK 15
Db 13 RIQGGGFAVTVIGK 27

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RESULT 12
US-09-886-149-66
; Sequence 66, Application US/09886149
; Publication No. US20030030442A1

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; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495.0001-04
; CURRENT APPLICATION NUMBER: US/09/886,149
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-886-149-66

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Query Match 100.0%; Score 77; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 RIQGGGFAVTVIGK 15
Db 13 RIQGGGFAVTVIGK 27

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RESULT 13
US-09-886-159-66
; Sequence 66, Application US/09886159
; Publication No. US20030030443A1
; GENERAL INFORMATION:
; APPLICANT: Guertler, Lutz G.
; APPLICANT: Eberle, Josef
; APPLICANT: Brunn, Albrecht V.
; APPLICANT: Knapp, Stefan
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
; FILE REFERENCE: 05495.0001-04
; CURRENT APPLICATION NUMBER: US/09/886,159
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: US/09/109,916
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: DE P 42 33 646.5
; PRIOR FILING DATE: 1992-10-06
; PRIOR APPLICATION NUMBER: DE P 42 35 718.7
; PRIOR FILING DATE: 1992-10-22
; PRIOR APPLICATION NUMBER: DE P 42 44 541.8
; PRIOR FILING DATE: 1992-12-30
; PRIOR APPLICATION NUMBER: DE P 43 18 186.4
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-886-159-66

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Query Match 100.0%; Score 77; DB 9; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.9e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 16 secs

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Db 13 RIQGGGRAFTVIGK 27

RESULT 14
US-09-810-310-2
; Sequence 2, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Bezofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-2

Query Match 100.0%; Score 77; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 25 RIQGGGRAFTVIGK 39

RESULT 15
US-09-810-310-3
; Sequence 3, Application US/09810310
; Patent No. US20020044948A1
; GENERAL INFORMATION:
; APPLICANT: Khleif, Samir N.
; APPLICANT: Bezofsky, Jay A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CO-STIMULATION OF
; TITLE OF INVENTION: IMMUNOLOGICAL RESPONSES TO PEPTIDE ANTIGENS
; FILE REFERENCE: 15280-415100US
; CURRENT APPLICATION NUMBER: US/09/810,310
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,396
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 39
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV PEPTIDE
; OTHER INFORMATION: ANTIGEN
US-09-810-310-3

Query Match 100.0%; Score 77; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.le-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQGGGRAFTVIGK 15
Db 25 RIQGGGRAFTVIGK 39

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OM protein - protein search, using sw model

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(without alignments)
27.584 Million cell updates/sec

Title: US-09-191-772A-2

Perfect score: 77
Sequence: 1 RIQGPGRFVTGK 15

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Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	77	100.0	15	1	US-08-218-025A-17
3	77	100.0	15	1	US-08-709-047-7
4	77	100.0	15	1	US-08-479-400-2
5	77	100.0	15	1	US-08-410-360-7
6	77	100.0	15	1	US-08-095-332-1
7	77	100.0	15	1	US-08-707-801A-7
8	77	100.0	15	1	US-08-709-006-7
9	77	100.0	15	1	US-08-711-175-7
10	77	100.0	15	1	US-08-488-252-27
11	77	100.0	15	2	US-08-021-879-2
12	77	100.0	15	2	US-07-760-530-1
13	77	100.0	15	2	US-07-950-571A-3
14	77	100.0	15	2	US-08-975-699-6
15	77	100.0	15	2	US-08-972-089-6
16	77	100.0	15	2	US-08-455-625-7
17	77	100.0	15	2	US-08-395-204-2
18	77	100.0	15	2	US-08-628-687-1
19	77	100.0	15	2	US-07-847-311A-1
20	77	100.0	15	2	US-08-986-234-13
21	77	100.0	15	2	US-08-986-234-28
22	77	100.0	15	3	US-08-492-076-22
23	77	100.0	15	3	US-08-493-071-25
24	77	100.0	15	4	US-08-480-332-1
25	77	100.0	15	4	US-08-455-685-7
26	77	100.0	15	4	US-08-060-988A-7
27	77	100.0	15	4	US-09-051-006-8

28 77 100.0 15 5 PCT-US92-10378-1 Sequence 1, Appli
29 77 100.0 15 5 PCT-US94-05142-7 Sequence 7, Appli
30 77 100.0 16 2 US-08-657-392-28 Sequence 28, Appli
31 77 100.0 16 2 US-08-251-472-2 Sequence 2, Appli
32 77 100.0 16 2 US-08-484-905-35 Sequence 35, Appli
33 77 100.0 16 3 US-08-481-985B-35 Sequence 35, Appli
34 77 100.0 16 3 US-09-248-082-2 Sequence 2, Appli
35 77 100.0 16 4 US-08-370-476-35 Sequence 35, Appli
36 77 100.0 16 4 US-08-992-877-15 Sequence 15, Appli
37 77 100.0 16 5 PCT-US94-02539-28 Sequence 28, Appli
38 77 100.0 18 1 US-08-015-770B-4 Sequence 4, Appli
39 77 100.0 20 1 US-08-121-054C-3 Sequence 3, Appli
40 77 100.0 20 1 US-08-488-252-28 Sequence 28, Appli
41 77 100.0 20 4 US-08-539-436-3 Sequence 4, Appli
42 77 100.0 21 2 US-08-452-503A-4 Sequence 4, Appli
43 77 100.0 21 2 US-08-453-745A-4 Sequence 4, Appli
44 77 100.0 21 2 US-08-470-419-25 Sequence 25, Appli
45 77 100.0 21 2 US-08-648-298-18 Sequence 18, Appli

ALIGNMENTS

RESULT 1
US-08-336-087-2
; Sequence 2, Application US/08336087
; Patent No. 5503829
; GENERAL INFORMATION:
; APPLICANT: Ladant, Daniel
; APPLICANT: Leclerc, Claude
; APPLICANT: Sebco, Peter
; APPLICANT: Ullmann, Agnes
; TITLE OF INVENTION: Recombinant Mutants for Inducing
; TITLE OF INVENTION: Specific Immune Responses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,087
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/011,644
; FILING DATE: 29-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495-0109-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-336-087-2

Query Match 100.0%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGGAFTVIGK 15
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Db 1 RIQGGGGAFTVIGK 15

RESULT 2
US-08-218-025A-17
; Sequence 17, Application US/08218025A
; Patent No. 5556744
; GENERAL INFORMATION:
; APPLICANT: Weiner, David B.
; APPLICANT: Ugen, Kenneth E.
; APPLICANT: Williams, William V.
; TITLE OF INVENTION: Methods and Compositions for Diagnosing
; TITLE OF INVENTION: and Treating Certain HIV Infected Patients
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: P.O. Box 457, 321 No. 5556744ristown Road
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/218.025A
; FILING DATE: 24-MAR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/891,451
; FILING DATE: 29-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST33A
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-218-025A-17

Query Match 100.0%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGGAFTVIGK 15
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Db 1 RIQGGGGAFTVIGK 15

RESULT 3
US-08-709-047-7
; Sequence 7, Application US/08709047
; Patent No. 5652333
; GENERAL INFORMATION:
; APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
; APPLICANT: Liming
; TITLE OF INVENTION: THE GC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,
; TITLE OF INVENTION: AND RELATED PEPTIDES AND TARGETING ANTIBODIES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.

QY 1 RIQGGGGAFTVIGK 15
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Db 1 RIQGGGGAFTVIGK 15

RESULT 4
US-08-479-400-2
; Sequence 2, Application US/08479400
; Patent No. 5679784
; GENERAL INFORMATION:
; APPLICANT: Ladtant, Daniel
; APPLICANT: Leclerc, Claude
; APPLICANT: Sebo, Peter
; APPLICANT: Ullmann, Agnes
; TITLE OF INVENTION: Recombinant Mutants for Inducing
; TITLE OF INVENTION: Specific Immune Responses
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,400
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/011,644
; FILING DATE: 29-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.

QY 1 RIQGGGGAFTVIGK 15
|||||
Db 1 RIQGGGGAFTVIGK 15

Query Match 100.0%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGGAFTVIGK 15
|||||
Db 1 RIQGGGGAFTVIGK 15

US-08-709-047-7

; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495-0109-01000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-479-400-2

Query Match 100.0%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQPGPGRAFTVIGK 15
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Db 1 RIQPGPGRAFTVIGK 15

RESULT 5
US-08-410-360-7

; Sequence 7, Application US/08410360
; Patent No. 5691447
; GENERAL INFORMATION:
; APPLICANT: Fung, Michael S.C., Sun, Bill N.C, Sun, Cecily R.Y., Kim, Young W., Yu,
; APPLICANT: Liming
; TITLE OF INVENTION: THE gC1q RECEPTOR, HIV-1 gp120 REGION BINDING THERETO,
; TITLE OF INVENTION: AND RELATED PEPTIDES AND TARGETING ANTIBODIES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/410,360
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TNX95-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (713) 664-2288
; TELEFAX: (713) 664-8914
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-410-360-7

Query Match 100.0%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQPGPGRAFTVIGK 15
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Db 1 RIQPGPGRAFTVIGK 15

RESULT 6
US-08-095-332-1
; Sequence 1, Application US/08095332
; Patent No. 5711947
; GENERAL INFORMATION:
; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Takahashi, Hidemi
; APPLICANT: Germain, Ronald N.
; TITLE OF INVENTION: METHOD TO INDUCE CYTOTOXIC T LYMPHOCYTES
; TITLE OF INVENTION: SPECIFIC FOR A BROAD ARRAY OF HIV-1 ISOLATES USING HYBRID
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolaah & Birch
; STREET: 301 N. Washington
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,332
; FILING DATE: 23-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/760,530
; FILING DATE: 18-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svenssen, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1173-354p
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345

; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: HIV-1
; INDIVIDUAL ISOLATE: IIIB
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..15
; OTHER INFORMATION: /label= peptide
; OTHER INFORMATION: /note= "synthetic peptide, sequence = residues 315
; OTHER INFORMATION: to 329 of HIV-1, isolate IIIB, gp160 envelope
; OTHER INFORMATION: glycoprotein."
US-08-095-332-1

Query Match 100.0%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQPGPGRAFTVIGK 15
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Db 1 RIQPGPGRAFTVIGK 15

RESULT 7
US-08-707-801A-7
; Sequence 7, Application US/08707801A
; Patent No. 5728814
; GENERAL INFORMATION:

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGAFVTVIGK 15
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Db 1 RIQGGGAFVTVIGK 15

RESULT 10

US-08-488-252-27
; Sequence 27, Application US/08488252
; Patent No. 5763160

GENERAL INFORMATION:

; APPLICANT: Chang Yi Wang
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND PROCESS
; OF USING SAME FOR THE DETECTION OF ANTIBODIES TO
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS (HIV) GP120 ENVELOPE
; TITLE OF INVENTION: PROTEIN, DIAGNOSIS OF AIDS AND PRE-AIDS CONDITIONS
; TITLE OF INVENTION: AND AS VACCINES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVE.
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

COMPUTER READABLE FORM:

; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,252
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,676
; FILING DATE: 07-Jun-1995
; APPLICATION NUMBER: 07/726,605
; FILING DATE: 09-July-1991
; APPLICATION NUMBER: 07/663,262
; FILING DATE: 01-Mar-1991
; APPLICATION NUMBER: 07/155,321
; FILING DATE: 12-Feb-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C. H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4004 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792

INFORMATION FOR SEQ ID NO: 27:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: Amino acids
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown

US-08-488-252-27

Query Match 100.0%; Score 77; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGAFVTVIGK 15
|||||

Db 1 RIQGGGAFVTVIGK 15

RESULT 11

US-08-021-879-2
; Sequence 2, Application US/08021879
; Patent No. 5817767

; GENERAL INFORMATION:
; APPLICANT: Graham P. Allaway
; APPLICANT: Paul J. Maddon
; TITLE OF INVENTION: SYNERGISTIC COMPOSITION OF CD4-BASED
; TITLE OF INVENTION: PROTEIN AND ANTI-HIV-1 ANTIBODY, AND
; TITLE OF INVENTION: METHODS OF USING SAME
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,879
; FILING DATE: 24-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 41189/JPM/AJM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOPUI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-021-879-2

Query Match 100.0%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGGAFVTVIGK 15
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Db 1 RIQGGGAFVTVIGK 15

RESULT 12

US-07-760-530-1
; Sequence 1, Application US/07760530
; Patent No. 5820865

GENERAL INFORMATION:

; APPLICANT: Berzofsky, Jay A.
; APPLICANT: Takahashi, Hidemi
; APPLICANT: Germain, Ronald N.
; TITLE OF INVENTION: METHOD TO INDUCE CYTOTOXIC T LYMPHOCYTES
; TITLE OF INVENTION: SPECIFIC FOR A BROAD ARRAY OF HIV-1 ISOLATES USING HYBRID
; TITLE OF INVENTION: SYNTHETIC PEPTIDES
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Kolash & Birch
; STREET: 301 N. Washington
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/07/760,530
; FILING DATE: 19910918
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1173-354p
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: HIV-1
; INDIVIDUAL ISOLATE: IIIB
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-15
; OTHER INFORMATION: /label= peptide
; OTHER INFORMATION: /note= "synthetic peptide, sequence = residues 315
; OTHER INFORMATION: to 329 of HIV-1, isolate IIIB, gp160 envelope
; OTHER INFORMATION: glycoprotein."
;
US-07-760-530-1

Query Match      100.0%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGPGRAFTVIGK 15
Db 1 RIQGGPGRAFTVIGK 15

RESULT 13
US-07-950-571A-3
; Sequence 3, Application US/07950571A
; Patent No. 5854400
; GENERAL INFORMATION:
; APPLICANT: Chang, Tse Wen, Fung, Michael S.C., Sun, Bill N.C., Sun, Cecily R.Y.
; APPLICANT: Chang, Nancy T.
; TITLE OF INVENTION: Monoclonal Antibodies which Neutralize HIV-1 Infection
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Tanox Biosystems, Inc.
; STREET: 10301 Stella Link Rd.
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Hi Density Diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: DOS, Version 3.30
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/950,571A
; FILING DATE: 19920922
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 5854400 07/767,533
; FILING DATE: 09/26/1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirabel, Eric P.
; REGISTRATION NUMBER: 31,211
; REFERENCE/DOCKET NUMBER: TNX87-11BBC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-664-2288

; APPLICATION NUMBER: US/07/760,530
; FILING DATE: 19910918
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30,330
; REFERENCE/DOCKET NUMBER: 1173-354p
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; ORGANISM: HIV-1
; INDIVIDUAL ISOLATE: IIIB
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1-15
; OTHER INFORMATION: /label= peptide
; OTHER INFORMATION: /note= "synthetic peptide, sequence = residues 315
; OTHER INFORMATION: to 329 of HIV-1, isolate IIIB, gp160 envelope
; OTHER INFORMATION: glycoprotein."
;
US-07-760-530-1

Query Match      100.0%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGGPGRAFTVIGK 15
Db 1 RIQGGPGRAFTVIGK 15

RESULT 14
US-08-975-699-6
; Sequence 6, Application US/08975699
; Patent No. 5858369
; GENERAL INFORMATION:
; APPLICANT: MATSUO, KAZUHIRO
; APPLICANT: CHUJO, YOSHITOMO
; APPLICANT: YAMAZAKI, AKIHIRO
; APPLICANT: HONDA, MITSUO
; APPLICANT: YAMAKAZI, SHUDO
; APPLICANT: TASAKA, HIROMICHI
; TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
; TITLE OF INVENTION: VACCINE
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/975,699
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/619,512
; FILING DATE: 29-MAR-1996
; APPLICATION NUMBER: PCT/JP95/01515
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 178462/1994
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-795-0X PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; STRAIN: HIV-1 (JAPAN)
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US-08-975-699-6

Query Match 100.0%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RIQGPGRAFVTIGK 15
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Db 1 RIQGPGRAFVTIGK 15

RESULT 15

US-08-972-089-6
; Sequence 6, Application US/08972089
; Patent No. 5885580
; GENERAL INFORMATION:
; APPLICANT: MATSUO, KAZUHIRO
; APPLICANT: CHUJO, YOSHITOMO
; APPLICANT: YAMAZAKI, AKIHIRO
; APPLICANT: HONDA, MITSUO
; APPLICANT: YAMAKAZI, SHUDO
; APPLICANT: TASAKA, HIROMICHI
; TITLE OF INVENTION: ANTI-AIDS SECRETORY RECOMBINANT BCG
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,089
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/975,699
; FILING DATE:
; APPLICATION NUMBER: PCT/JP95/01515
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 178462/1994
; FILING DATE: 29-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-795-OX PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
; STRAIN: HIV-1 (JAPAN)
US-08-972-089-6

Query Match 100.0%; Score 77; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 RIQGPGRAFVTIGK 15

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Job time : 17 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: March 10, 2003, 17:41:23 ; Search time 36 Seconds
(without alignments)
55.521 Million cell updates/sec

Title: US-09-191-772A-2

Perfect score: 77

Sequence: 1 RIQGPGRFAVTICK 15

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	15	9 AAP82095	Env-K1 peptide.
2	77	100.0	15	10 AAP91228	Peptide comprising
3	77	100.0	15	13 AAR21343	Sequence of antigen
4	77	100.0	15	14 AAR32207	Sequence of peptide
5	77	100.0	15	14 AAR38187	V3 loop peptide D4
6	77	100.0	15	15 AAR51619	V3 loop region of
7	77	100.0	15	16 AAR74603	HIV-1 variable loop
8	77	100.0	15	16 AAR68789	Cytotoxic T lympho
9	77	100.0	15	16 AAR66414	HIV-1 IIB peptide
10	77	100.0	15	17 AAW07931	Gp120 peptide p18p

11	77	100.0	15	17 AAW05535	HIV-1 gp120 peptid
12	77	100.0	15	17 AAR52007	HIV-1 V3 loop epit
13	77	100.0	15	17 AAR92033	Hydrophilic peptid
14	77	100.0	15	18 AAW24219	CD4+ T-lymphocyte
15	77	100.0	15	18 AAW22031	Antigenic human im
16	77	100.0	15	18 AAW10348	HIV epitope env p1
17	77	100.0	15	19 AAW76898	Fusion immunoglobu
18	77	100.0	15	19 AAW54929	HIV gp120 envelope
19	77	100.0	15	19 AAW40316	HIV-1 IIB gp120 p
20	77	100.0	15	19 AAW39275	HIV-1 synthetic pe
21	77	100.0	15	20 AAY24466	HIV peptide R15K-1
22	77	100.0	15	20 AAY25189	HIV protein gp160
23	77	100.0	15	20 AAY25204	HIV V3 peptide fra
24	77	100.0	15	20 AAY05356	HIV-1 CLOVAC pepti
25	77	100.0	15	20 AAY06896	Sequence of gp120I
26	77	100.0	15	20 AAY04680	HIV-1 gp120 amino
27	77	100.0	15	20 AAW87620	Epitope of HIV-1 g
28	77	100.0	15	20 AAW72821	HIV-1 gp120 monocl
29	77	100.0	15	21 AAY85591	HIV related peptid
30	77	100.0	15	21 AAB15875	Human chemokine de
31	77	100.0	15	21 AAY83916	HIV-1 env T-cell e
32	77	100.0	15	21 AAY66439	HLA-A2-binding HIV
33	77	100.0	15	21 AAY66455	HLA-A3-binding HIV
34	77	100.0	15	22 AAB92345	Virus related pept
35	77	100.0	15	22 AAB92348	HIV gp120 V3 loop
36	77	100.0	15	22 AAB68601	HIV-1 P18IIB pept
37	77	100.0	15	23 AAB68654	HIV-1 P18 based pe
38	77	100.0	15	23 AAB68663	HIV CTL epitope pe
39	77	100.0	15	23 AAW97690	HIV epitope HIV-1
40	77	100.0	15	23 AAW96031	Human immunodefici
41	77	100.0	15	23 AAE15743	HIV peptide ENV 31
42	77	100.0	16	13 AAR24939	MHC binding peptid
43	77	100.0	16	19 AAW68326	Altered MHC determ
44	77	100.0	16	21 AAY68203	Altered MHC determ
45	77	100.0	16	21 AAY52857	Altered MHC determ

ALIGNMENTS

RESULT 1

AAP82095

ID AAP82095 standard; peptide; 15 AA.

XX AAP82095;

DT 17-DEC-2001 (updated)

DT 29-OCT-1990 (first entry)

XX Env-K1 peptide.

XX Env-K1; gp160 Env protein; T-cell cytotoxicity; HIV.

OS synthetic.

XX USN7148692-N.

XX 02-AUG-1988.

XX 26-JAN-1988; 88US-0192059.

XX 26-JAN-1988; 88US-0148692.

XX (USSH) US DEPT HEALTH AND HUMAN.

XX (USDC) US SEC OF COMMERCE.

PI Berzofsky J, Takahashi H, Hosmalin A, Germain R, Moss B; WPI; 1988-264280/37.

XX Synthetic peptide corresp. to HIV gp 160 Env sequence -

PT which elicits cytotoxicity by T cells against HIV and

PT proliferation of HIV-specific T cells

DT 17-DEC-2001 (updated)
 DT 07-JUN-1993 (first entry)
 DE Sequence of peptide which corresp.to AA residues 315-329 of the V3
 DE loop of the gp160 envelope glycoprotein in HIV-1 strain MN.
 XX V3 loop; envelope glycoprotein; gp160; HIV-1; prophylaxis;
 KW immunotherapy.
 XX Human immunodeficiency virus (HIV-1) isolate IIIB.
 OS USN760530-N.
 PN USN760530-N.
 XX 15-DEC-1992.
 PD 18-SEP-1991; 91US-0760530.
 PF 18-SEP-1991; 91US-0760530.
 PR (USSH) US DEPT HEALTH & HUMAN SERVICE.
 PA Berzofsky JA, Germain RN, Takahashi H;
 XX WPI; 1993-058406/07.
 DR Peptide(s) corresponding to the V3 loop of gp=160 of HIV-1 -
 XX elicit cytotoxic T lymphocyte(s) active against broad range of
 PT HIV-1 isolate(s)
 PT Example; Page 19; 41pp; English.
 PS The peptide corresponds to amino acid residues numbered 315-329 in
 CC the V3 loop of the envelope glycoprotein gp160 of human
 CC immunodeficiency virus (HIV-1), as numbered by Ratner in the strain
 CC MN. It is useful for the prophylaxis or immunotherapy of HIV-1
 CC infection. It elicits an immunised subject cytotoxic T lymphocyte
 CC (CTL) activity against the corresp. clinical isolate of HIV-1.
 CC (Note: Revised entry submitted to correct the patent number format of
 CC US Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/ntis_us.html.)
 XX Sequence 15 AA;
 SQ Query Match 100.0%; Score 77; DB 14; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQRGPGRAFTVIGK 15
 Db 1 RIQRGPGRAFTVIGK 15
 RESULT 5
 ID AAR38187 standard; peptide; 15 AA.
 XX AAR38187;
 AC AAR38187;
 XX 12-OCT-1993 (first entry)
 DT V3 loop peptide D44 (R15K).
 DE gp120; HIV-1; cytotoxic T-lymphocyte; CTL; T-helper;
 KW AIDS; infection.
 XX Human immunodeficiency virus-1 strain IIIB.
 OS WO9310816-A.
 PN 10-JUN-1993.
 PD 02-DEC-1992; 92WO-US10378.
 PF

XX 02-DEC-1991; 91US-0800932.
 PR 16-SEP-1992; 92US-0945865.
 XX (TEXA) UNIV TEXAS SYSTEM.
 PA Arlinghaus RB, Nehete PN, Platsoucas CD, Sastry JK;
 XX WPI; 1993-196739/24.
 DR Peptide composition for treating and preventing viral infections
 XX - comprise CTL-inducing epitope and HIV infection-inhibiting
 PT sequence or T helper cell-inducing sequence
 PT Claim 13 + 19; Page 94-95; 130pp; English.
 PS HIV gp120 V3 loop-derived peptides (AAR38170-87) are successful in
 CC generating CTL responses, esp. peptide R15K (AAR38187); the T-helper
 CC cell-inducing peptide includes the sequence C19A (AAR38164);
 CC HIV infection-inhibiting peptides are given in AAR38188-206, and are
 CC esp. peptides R15K, N24G, E13V, R8K, T13Q and H13N (AAR38165-69).
 CC The peptides may also be derived from an influenza virus protein or
 CC a sendai virus protein (AAR41014-15).
 CC It was observed that peptide R15K (amino acids 315-329), with sequences
 CC derived from the V3 loop of HIV-1 IIIB, inhibits HIV-1 infection of
 CC primary human T cells by 92% at 1 microg/ml (ca. 0.4-0.6 microM).
 XX Sequence 15 AA;
 SQ Query Match 100.0%; Score 77; DB 14; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQRGPGRAFTVIGK 15
 Db 1 RIQRGPGRAFTVIGK 15
 RESULT 6
 ID AAR51619 standard; Protein; 15 AA.
 XX AAR51619;
 AC AAR51619;
 XX 21-OCT-1994 (first entry)
 DT V3 loop region of gp120 of HIV.
 DE gp 120; HIV epitope;
 KW Human Immunodeficiency Virus fusion polypeptide.
 XX Human Immunodeficiency Virus.
 OS WO9406469-A.
 PN 31-MAR-1994.
 PD 18-SEP-1992; 92WO-US07966.
 PF 18-SEP-1992; 92WO-US07966.
 PR (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
 PA Altman A, Baier GJ;
 XX WPI; 1994-118166/14.
 DR New fusion polypeptide of antigen binding domain and HIV epitope
 PT - useful as vaccine for treatment or prevention of HIV infection,
 PT ensures efficient focusing of epitopes on surface of antigen
 PT presenting cells
 XX Example 1; Page 24; 39pp; English.
 PS

XX AAR51619 shows a region of the V3 loop (residues 315-329) of the
 CC envelope glycoprotein, gp120, of HIV-1. It represents an epitope
 CC which forms part of a hybrid-fusion polypeptide with a
 CC Fab fragment of an IgG Fab fragment. The polypeptide is capable of
 CC presenting the epitope to antigen presenting cells.
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

QY 1 RIQGPGRFAFTVIGK 15
 |||||
 Db 1 RIQGPGRFAFTVIGK 15

RESULT 7

AAR74603
 ID AAR74603 standard; peptide; 15 AA.

XX AC AAR74603;

XX DT 01-NOV-1995 (first entry)

XX DE HIV-1 variable loop residues 308-322.

XX KW Mab 5023; variable V3 loop; HIV-1; human immunodeficiency virus;
 KW cancer antigen; monoclonal antibody.

XX OS Human immunodeficiency virus I.

XX PN WO9510777-A.

XX PD 20-APR-1995.

XX PF 14-OCT-1994; 94WO-US11754.

XX PR 15-OCT-1993; 93US-0138141.

XX PA (RAKO/) RAKOWICZ-SZULCZYNSKA E M.

XX PA (RAKO/) RAKOWICZ-SZULCZYNSKA E M.

XX PI Rakowicz-szulczynska EM;

XX PS WPI; 1995-178531/23.

XX PT Detection of HIV-1 cross-reactive breast carcinoma-associated
 PT antigens - for diagnosis and anti-sense therapy of breast and
 PT gynaecological cancers.

XX PS Disclosure; Page 48; 71pp; English.

XX CC Mab 5023 was developed against AA residue 308-322 of the variable
 CC loop of HIV-1 (AAR74603). Mab 5023 binds to the epitope GRAF. G
 CC preceding RAF is believed to critical for internalization. Mab 5023
 CC recognised p160, p120, p42 and p24 in cancer cells. AAR74603
 CC competitively blocked binding of the Mab to the cancer antigens,
 CC indicating that at least the epitope GRAF, which is recognised by
 CC the Mab, must also be present in cancer antigens.
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

QY 1 RIQGPGRFAFTVIGK 15
 |||||
 Db 1 RIQGPGRFAFTVIGK 15

RESULT 8

AAR68789
 ID AAR68789 standard; peptide; 15 AA.

XX AC AAR68789;

XX DT 23-AUG-1995 (first entry)

XX DE Cytotoxic T lymphocyte epitope 46 derived from env gp120 protein.

XX KW cytotoxic T lymphocyte; epitope; antigen; pathogenic; nef; gag; pol;
 KW env; gp120; gp41; HIV; cell-mediated immunity;
 KW human immunodeficiency virus; class I restricted.

XX OS Human immunodeficiency virus.

XX PN WO9428871-A.

XX PD 22-DEC-1994.

XX PF 07-JUN-1994; 94WO-US06394.

XX PR 07-JUN-1993; 93US-0072718.

XX PA (ENDO-) ENDOCON INC.

XX PI Leonard RJ;

XX PS WPI; 1995-036067/05.

XX PT Implant for sustained release of pathogen-associated antigen -
 PT forming chronic inflammatory site producing cytotoxic
 PT T-lymphocytes lysing infected cells, esp. for treating AIDS

XX PS Disclosure; Page 12; 35pp; English.

XX CC AAR68744-805 are cytotoxic T lymphocyte (CTL) class I and II restricted
 CC epitopes derived from human immunodeficiency virus proteins. AAR68789
 CC corresponds to amino acid residues 308-322 of the env gp120 protein.
 CC These antigens are examples of peptides that can be used with an
 CC immunogenic implant. The implant is associated with an antigen
 CC associated with a pathogen and used to form a local 'factory' for prodn. of
 CC chronic inflammation site which acts as a local 'factory' for prodn. of
 CC CTL's which lyse cells infected with a specific pathogen. The expanded
 CC set of pathogen-specific CTL's can eradicate or prevent development of
 CC infection, and can also be used to treat or arrest the development of
 CC cancers associated with infection.
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05; Indels 0; Gaps 0;
 Matches 15; Conservative 0; Mismatches 0;

QY 1 RIQGPGRFAFTVIGK 15
 |||||
 Db 1 RIQGPGRFAFTVIGK 15

RESULT 9

AAR66414
 ID AAR66414 standard; peptide; 15 AA.

XX AC AAR66414;

XX DT 03-AUG-1995 (first entry)

XX DE HIV-1 IIIB peptide 18.

XX KW T cell helper site; cytotoxic T cell response; neutralising antibody;
 KW human immunodeficiency virus type 1; envelope glycoprotein gp120;
 KW cluster peptide; principal neutralising determinant; IIIB isolate.

XX

OS Synthetic.
 PN WO9426785-A.
 XX
 PD 24-NOV-1994.
 XX
 PF 13-MAY-1994; 94WO-US05142.
 XX
 PR 14-MAY-1993; 93US-0060988.
 XX
 PS (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA (USSH) US SEC DEPT HEALTH.
 XX
 PI Ahlers JD, Berzofsky JA, Nara P, Pendleton CD, Shirai M;
 XX WPI; 1995-006707/01.
 XX
 DR Polypeptide inducing helper T cell, cytotoxic T cell and
 PT antibodies responses - to target antigen in hosts of different
 PT MHC haplotypes, esp. for therapeutic or prophylactic vaccines
 PT against HIV.
 XX
 PS Example 1; Page 33; 120pp; English.
 XX
 CC Synthetic peptides spanning multideterminant regions from the HIV
 CC envelope protein gp160 have been designed and are designated cluster
 CC peptides (CPIUS). These peptides each consist of a cluster of
 CC overlapping determinants and are known to induce in vitro T cell
 CC proliferation and cytokine production in mice and humans of multiple
 CC MHC types. The cluster peptides were co-linearly synthesised at the
 CC N-terminus of an immunodominant CTL determinant, Peptide 18 (AAR66414),
 CC corresp. to part of the gp160 V3 loop and principal neutralising
 CC determinant region of HIV-1 IIIB isolate.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 77; DB 16; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIORGPGRAFTVIGK 15
 DB |||||
 1 RIORGPGRAFTVIGK 15
 RESULT 10
 AAW07931
 ID AAW07931 standard; peptide; 15 AA.
 XX
 AC AAW07931;
 XX
 DT 31-JAN-1997 (first entry)
 XX
 DE gp120 peptide p18p.
 XX
 KW HIV; gp120; HIV-IIIB strain; HIV-1 transmission; foetal transmission;
 KW neutralising antibody; passive immunisation; anti-idiotypic antibody;
 KW gp41; vaccine; active immunotherapy.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN US5556744-A.
 XX
 PD 17-SEP-1996.
 XX
 PF 24-MAR-1994; 94US-0218025.
 XX
 PR 24-MAR-1994; 94US-0218025.
 PR 29-MAY-1992; 92US-0891451.
 XX
 PA (UYPE-) UNIV PENNSYLVANIA.
 PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX

PI Ugen KE, Weiner DB, Williams WV;
 XX
 DR WPI; 1996-432980/43.
 XX
 PT Determining the likelihood of maternal transmission of HIV-1 to
 PT foetus - by measuring maternal reactivity with specific gp120 and
 PT gp41 derived peptide(s), also used for diagnosing HIV in infants
 XX
 PS Example 2; Column 18; 63pp; English.
 XX
 CC This sequence represents a HIV gp120 peptide that can be used in the
 CC method of the invention. The method of the invention is for determining
 CC whether or not a mother will transmit HIV-1 to a foetus. The method
 CC comprises incubating a sample from the HIV-infected mother, with a
 CC collection of HIV peptides. The HIV peptides includes at least one of
 CC the gp120 sequences (such as AAW07909-W07917), and at least one HIV gp41
 CC derived peptide (see AAW07918-W07928). The number of peptides that
 CC react with the sample is determined, and this number is compared with a
 CC standard that shows pattern reactivity for a patient of transmission
 CC status. A non-transmissible HIV sample is indicated if the test sample
 CC reacts with twice as many peptides as the standard. The method detects
 CC the presence of neutralising antibodies that protect against mother to
 CC infant transmission of HIV. These sequences can also be used in
 CC vaccines to protect against transmission. Antibodies against these
 CC sequences can be used for passive immunisation, and to generate
 CC anti-idiotypic antibodies for use in vaccines or active immunotherapy.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 77; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIORGPGRAFTVIGK 15
 DB |||||
 1 RIORGPGRAFTVIGK 15
 RESULT 11
 AAW05535
 ID AAW05535 standard; Peptide; 15 AA.
 XX
 AC AAW05535;
 XX
 DT 17-JAN-1997 (first entry)
 XX
 DE HIV-1 gp120 peptide (aa308-322).
 XX
 KW gC1q receptor; gC1q-R; HIV-1; gp120; immunogen; vaccine.
 XX
 OS Human immunodeficiency virus type 1 strain HXB2R.
 XX
 PN WO9630400-A1.
 XX
 PD 03-OCT-1996.
 XX
 PF 22-MAR-1996; 96WO-US03905.
 XX
 PR 24-MAR-1995; 95US-0410360.
 XX
 PA (TANO-) TANOX BIOSYSTEMS INC.
 XX
 PI Fung MSC, Kim YW, Sun BNV, Sun CRY, Yu L;
 XX WPI; 1996-455274/45.
 XX
 DR New gC1q receptor-based, HIV-1 gp 120 binding peptide(s) - for
 PT preventing and treating HIV-1 infection
 XX
 PS Claim 10; Page 49; 53pp; English.
 XX
 CC A peptide (AAW05535) corresponds to amino acids 308-322 of the V3
 CC region of gp120 from HIV-1 strain HXB2R2. It was used to examine

CC the binding of gC1q receptor (gC1q-R) (see also AAW05534) to HIV-1
 CC gp120. Anti-HIV-1 gp120 V3 domain murine monoclonal antibody
 CC BAF123 was able to react with gp120 bound to gC1q-R, showing that
 CC the binding of gC1q-R to gp120 does not involve the V3 region of
 CC gp120; the binding site was localised to amino acids 444-459 (see
 CC also AAW05533) of gp120.
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGPGRFAVTVIGK 15
 |||||
 Db 1 RIQGPGRFAVTVIGK 15

RESULT 12
 AAR92007
 ID AAR92007 standard; Protein; 15 AA.
 XX
 AC AAR92007;
 XX
 DT 27-SEP-1996 (first entry)
 XX
 DE HIV-1 V3 loop epitope, for insertion in Mycobacterium alpha antigen.
 XX
 KW Mycobacterium bovis BCG; AIDS vaccine; surface protein;
 KW alpha antigen; Human immunodeficiency virus type 1; fusion protein;
 KW gp120 epitope; V3 loop.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PI WO9604009-A1.
 PN
 PD 15-FEB-1996.
 XX
 PF 31-JUL-1995; 95WO-JP01515.
 XX
 PR 29-JUL-1994; 94JP-0178462.
 XX

(AJIN) AJINOMOTO CO INC.
 (NINA-) JAPAN AGENCY NAT INST HEALTH.
 XX
 PI Chujo Y, Honda M, Matsuo K, Tasaka H, Yamazaki A;
 PI Yamazaki S;
 XX
 WPI; 1996-129127/13.
 DR N-PSDB; AAT16048, AAT16049.
 XX
 PT BCG containing vaccine secretes chimeric protein containing foreign
 PT antigen - has enhanced immunogenicity and antigenicity esp. when
 PT used as an anti-AIDS vaccine
 XX
 PS Example 2; Page 17; 56pp; Japanese.
 XX

CC Antigenic peptides can be inserted into the alpha-antigen sequence
 CC of a Mycobacterium and secreted from an appropriately transformed
 CC M.bovis BCG cell. The resulting chimeric antigen has greatly
 CC enhanced antigenicity and immunogenicity and is recognised in vivo
 CC by B-cells which recognise the alpha-antigen. The present sequence
 CC is that of a HIV-1 gp120 V3 loop epitope which was incorporated
 CC into the alpha antigen. M.bovis BCG cells secreting a
 CC chimeric protein comprising the epitope sequence are useful as
 CC anti-AIDS vaccines.
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGPGRFAVTVIGK 15
 |||||
 Db 1 RIQGPGRFAVTVIGK 15

QY 1 RIQGPGRFAVTVIGK 15
 |||||
 Db 1 RIQGPGRFAVTVIGK 15
 RESULT 13
 AAR92033
 ID AAR92033 standard; peptide; 15 AA.
 XX
 AC AAR92033;
 XX
 DT 29-MAY-1996 (first entry)
 XX
 DE Hydrophilic peptide for epimorphin modification (5).
 XX
 KW Epimorphin; human; mouse; wound; burn; epithelial tissue;
 KW diagnosis; treatment; morphogenetic abnormality; cosmetic;
 KW hair growth stimulator.
 XX
 OS Synthetic.
 XX
 PN EP698666-A2.
 XX
 PD 28-FEB-1996.
 XX
 PF 20-JUN-1995; 95EP-0304270.
 XX
 PR 31-MAR-1995; 95JP-0099980.
 PR 21-JUN-1994; 94JP-0162874.
 PR 31-MAR-1995; 95JP-0099979.
 XX
 PA (SUME) SUMITOMO ELECTRIC IND CO.
 XX
 PI Hirai Y, Koshida S, Oka Y;
 XX
 WPI; 1996-118213/13.
 DR
 XX
 PT Novel polypeptide containing an epimorphin functional domain - has
 PT possible benefits in epithelial tissue treatments, e.g. burns and
 PT for artificial organs
 XX
 PS Claim 8; Page 57; 62pp; English.
 XX
 CC New polypeptides contain a first portion of 5-99 amino acids joined
 CC to a second portion contg. at least a functional domain of
 CC epimorphin. The first portion may be selected from the peptides
 CC given in AAR92029 to AAR92036. The second portion may be full-length
 CC epimorphin (see AAR92037 to AAR92042 for human and mouse epimorphins).
 CC Fragments of epimorphins given in AAT16083 to AAT16090 are used in the
 CC prodn. of modified epimorphins.
 CC The modified epimorphins are useful for the development of diagnosis
 CC and treatment of morphogenetic abnormalities of epithelial tissue or
 CC novel remedies for wounds, eg burns, after surgery and for artificial
 CC organs. They may also be used as components of cosmetics, hair
 CC growth stimulators, etc.
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 77; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RIQGPGRFAVTVIGK 15
 |||||
 Db 1 RIQGPGRFAVTVIGK 15

RESULT 14
 AAW24219
 ID AAW24219 standard; peptide; 15 AA.
 XX
 AC AAW24219;
 XX

DT 17-MAR-1998 (first entry)
 XX CD4+ T-lymphocyte epitope to HIV-1 V3 loop derived peptide V3-LAI-P18.
 DE T-lymphocyte epitope; diagnosis; antigen; infectious disease;
 XX delayed-type hypersensitivity assay; vaccine development.
 KW Synthetic.
 XX Human immunodeficiency virus.
 OS WO9727462-A2.
 XX 31-JUL-1997.
 XX 27-JAN-1997; 97WO-US01084.
 XX 26-JAN-1996; 96US-0010679.
 XX (USSA) US DEPT ARMY GOVERNMENT US ARMY MEDICAL.
 XX Brix DL, Sitz KV;
 XX WPI; 1997-393814/36.
 XX Peptide fragments containing antigen epitope(s) used to trace
 PT diseases - used in a delayed-type hypersensitivity assay, for in
 PT vivo mapping of human T-lymphocyte epitope(s) e.g. for diagnosis,
 PT vaccine development etc
 XX Disclosure; Page 6; 14pp; English.
 XX Peptide fragments AAW24217-20 were used to demonstrate a new method
 CC of tracing sources of infectious diseases. The method comprises
 CC preparing a short (9-50 amino acid) peptide containing at least one
 CC non-conserved epitope of an organism, injecting a composition containing
 CC the peptide intradermally into a test subject in a delayed-type
 CC hypersensitivity (DTH) assay and observing the injection site at
 CC intervals for induration. In this example CD4+ T-lymphocyte
 CC epitopes to the HIV-1 V3 loop were mapped by existing in vitro technique
 CC for two existing HIV infected individuals and used to design peptides
 CC AAW24217-20. The method allows the T-lymphocyte epitopes of a large
 CC antigen to be determined in vivo in humans. The method is useful in
 CC medicine e.g. in diagnosis, monitoring and treatment design for
 CC infectious disease exposure, active autoimmune disease, allergic diseases
 CC and malignancy. It is especially useful for tracing infectious diseases
 CC e.g. HIV, particularly when a sequence is present only in certain strains
 CC of an organism, and developing suitable vaccines. Vaccinated individuals
 CC can also be tested to verify protection against a particular strain.
 CC The method allows in vivo mapping of T-lymphocyte epitopes, not
 CC previously possible. The method is simpler, more rapid and more
 CC sensitive. It can also be applied in a variety of environments e.g.
 CC undeveloped regions since specialist equipment is not required.
 XX Sequence 15 AA;
 SQ Query Match 100.0%; Score 77; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQPGGRAFTVIGK 15
 |||||
 Db 1 RIQPGGRAFTVIGK 15
 |||||
 Search completed: March 10, 2003, 17:51:12
 Job time : 37 secs

XX Antigenic peptide; human papillomavirus; MAGE gene; BAGE-1 peptide; P18;
 KW human immunodeficiency virus; cancer antigen; tyrosinase; signal protein;
 KW anthrax lethal factor; LF; toxin; cationic fusion peptide; translocation;
 XX gene therapy; polycationic affinity handle; therapeutic protein; LFN.
 OS Human immunodeficiency virus.
 XX WO9723236-A1.
 XX 03-JUL-1997.
 XX 13-DEC-1996; 96WO-US20463.
 XX 07-JUN-1996; 96US-0019275.
 XX 13-DEC-1995; 95US-0008518.
 XX (HARD) HARVARD COLLEGE.
 XX Ballard JD, Blanke SR, Collier RJ, Lyszak EL, Milne JC;
 PI Starnbach MN;
 XX WPI; 1997-350782/32.
 XX Introducing therapeutic proteins, especially antigens, into cells
 PT using toxin molecules and/or polycationic handles for delivery
 PT Claim 15; Page 36; 67pp; English.
 XX This is the antigenic human immunodeficiency virus peptide P18. This
 CC antigenic compound can be introduced into the cytoplasm of a cell by a
 CC new method where the cell is contacted with a fusion molecule comprising
 CC a delivery molecule. The delivery molecule can either be a polycationic
 CC affinity handle, LFN (the protective antigen binding domain of anthrax
 CC lethal factor) or a toxin delivery molecule related to LFN. The antigenic
 CC compound is linked to either of the delivery molecules by a covalent
 CC bond. The B moiety of a toxin enhances delivery of the antigenic compound
 CC into a cell. The anthrax toxin system of the invention eliminates the
 CC need to generate fusion proteins with a toxin B moiety, which alleviates
 CC problems associated with incorrect folding of lengthy fusion proteins.
 CC Small cationic fusion peptides substituted for LFN may reduce the
 CC possibility of steric interference with the biological activity of the
 CC translocated protein. The method is used for the introduction of
 CC antigens, e.g. MHC class I antigens or any other therapeutic protein,
 CC e.g. toxin molecules, apoptosis-inducing molecules or signalling
 CC proteins into the cells.
 XX Sequence 15 AA;
 SQ Query Match 100.0%; Score 77; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQPGGRAFTVIGK 15
 |||||
 Db 1 RIQPGGRAFTVIGK 15
 |||||
 Search completed: March 10, 2003, 17:51:12
 Job time : 37 secs

DT 17-MAR-1998 (first entry)
 XX CD4+ T-lymphocyte epitope to HIV-1 V3 loop derived peptide V3-LAI-P18.
 DE T-lymphocyte epitope; diagnosis; antigen; infectious disease;
 XX delayed-type hypersensitivity assay; vaccine development.
 KW Synthetic.
 XX Human immunodeficiency virus.
 OS WO9727462-A2.
 XX 31-JUL-1997.
 XX 27-JAN-1997; 97WO-US01084.
 XX 26-JAN-1996; 96US-0010679.
 XX (USSA) US DEPT ARMY GOVERNMENT US ARMY MEDICAL.
 XX Brix DL, Sitz KV;
 XX WPI; 1997-393814/36.
 XX Peptide fragments containing antigen epitope(s) used to trace
 PT diseases - used in a delayed-type hypersensitivity assay, for in
 PT vivo mapping of human T-lymphocyte epitope(s) e.g. for diagnosis,
 PT vaccine development etc
 XX Disclosure; Page 6; 14pp; English.
 XX Peptide fragments AAW24217-20 were used to demonstrate a new method
 CC of tracing sources of infectious diseases. The method comprises
 CC preparing a short (9-50 amino acid) peptide containing at least one
 CC non-conserved epitope of an organism, injecting a composition containing
 CC the peptide intradermally into a test subject in a delayed-type
 CC hypersensitivity (DTH) assay and observing the injection site at
 CC intervals for induration. In this example CD4+ T-lymphocyte
 CC epitopes to the HIV-1 V3 loop were mapped by existing in vitro technique
 CC for two existing HIV infected individuals and used to design peptides
 CC AAW24217-20. The method allows the T-lymphocyte epitopes of a large
 CC antigen to be determined in vivo in humans. The method is useful in
 CC medicine e.g. in diagnosis, monitoring and treatment design for
 CC infectious disease exposure, active autoimmune disease, allergic diseases
 CC and malignancy. It is especially useful for tracing infectious diseases
 CC e.g. HIV, particularly when a sequence is present only in certain strains
 CC of an organism, and developing suitable vaccines. Vaccinated individuals
 CC can also be tested to verify protection against a particular strain.
 CC The method allows in vivo mapping of T-lymphocyte epitopes, not
 CC previously possible. The method is simpler, more rapid and more
 CC sensitive. It can also be applied in a variety of environments e.g.
 CC undeveloped regions since specialist equipment is not required.
 XX Sequence 15 AA;
 SQ Query Match 100.0%; Score 77; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.7e-05;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RIQPGGRAFTVIGK 15
 |||||
 Db 1 RIQPGGRAFTVIGK 15
 |||||
 Search completed: March 10, 2003, 17:51:12
 Job time : 37 secs

RESULT 15
 AAW22031
 ID AAW22031 standard; peptide; 15 AA.
 XX AAW22031;
 AC AAW22031;
 XX 20-FEB-1998 (first entry)
 DT Antigenic human immunodeficiency virus peptide P18.
 XX

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